

**AMENDMENTS TO THE CLAIMS:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**LISTING OF CLAIMS:**

Claim 1 (Withdrawn) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in a plant cell, comprising the step of introducing into said plant cell a chimeric DNA comprising the following operably linked parts:

- a) a promoter, operative in said plant cell;
- b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences,
  - wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence that is identical to at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest,
  - and wherein the second of said annealing RNA sequences comprises an antisense sequence that is identical to at least 20 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest,
  - and wherein said DNA region comprises an intron heterologous to said sense sequence; and
- c) a DNA region involved in transcription termination and polyadenylation.

Claim 2 (Withdrawn) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in a plant cell, comprising the step of introducing into said plant cell a chimeric DNA comprising the following operably linked parts:

- a) a promoter, operative in said plant cell;

- b) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising
  - i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest; and
  - ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 20 consecutive nucleotides of the sense sequence basepair with said at least 20 consecutive nucleotides of the antisense sequence,

and wherein said DNA region comprises an intron heterologous to said sense nucleotide sequence; and

- c) a DNA region involved in transcription termination and polyadenylation.

Claim 3 (Withdrawn) The method of claim 2, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequence.

Claim 4 (Withdrawn) The method of claim 2, wherein said sense nucleotide sequence comprises at least about 550 consecutive nucleotides having 100% sequence identity with at least about 550 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest.

Claim 5 (Withdrawn) The method of claim 2, wherein said nucleic acid of interest is a gene integrated in the genome of said plant cell.

Claim 6 (Previously Presented) The method of claim 5, wherein said gene is an endogenous gene.

Claim 7 (Withdrawn) The method of claim 5, wherein said gene is a foreign transgene.

Claim 8 (Withdrawn) The method of claim 2, wherein said chimeric DNA is stably integrated in the genome of said plant cell.

Claim 9 (Withdrawn) The method of claim 2, wherein said nucleic acid of interest is comprised in the genome of an infecting virus.

Claim 10 (Withdrawn) The method of claim 9, wherein said infecting virus is an RNA virus.

Claim 11 (Canceled).

Claim 12 (Withdrawn) The method of claim 2, wherein said plant cell is comprised within a plant.

Claims 13-21 (Canceled).

Claim 22 (Previously Presented) A plant cell, comprising a nucleic acid of interest, which is normally capable of being phenotypically expressed, further comprising a chimeric DNA molecule comprising the following operably linked parts:

- a) a promoter, operative in said plant cell;
- b) a DNA region, which when transcribed, yields an RNA molecule with at least one RNA region with a nucleotide sequence comprising
  - i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of the nucleic acid of interest; and
  - ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of

said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence,

and wherein said DNA region comprises an intron heterologous to said sense nucleotide sequence; and

c) a DNA region involved in transcription termination and polyadenylation.

Claims 23-25 (Canceled).

Claim 26 (Previously presented) A plant comprising the plant cell of claim 22.

Claims 27-39 (Canceled).

Claim 40 (Withdrawn) The method of claim 2, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 41 (Canceled).

Claim 42 (Previously presented) The plant cell of claim 22, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 43 (Withdrawn) The method of claim 2, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive

nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 44 (Previously Presented) The method of claim 2, wherein said sense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with at least 100 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with the complement of said at least 100 consecutive nucleotides of said sense nucleotide sequence.

Claim 45 (Canceled).

Claim 46 (Previously Presented) The method of claim 43 wherein said intron is located between the DNA region encoding said sense nucleotide sequence and the DNA region encoding said antisense nucleotide sequence.

Claims 47-49 (Canceled).

Claim 50 (Withdrawn) The method of claim 44, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claims 51-52 (Canceled).

Claim 53 (Previously Presented) The plant cell of claim 22, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 54 (Previously Presented) The plant cell of claim 22, wherein said sense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with at least 100 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with the complement of said at least 100 consecutive nucleotides of said sense nucleotide sequence.

Claim 55 (Canceled).

Claim 56 (Previously Presented) The plant cell of claim 53, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 57 (Canceled).

Claim 58 (Previously Presented) The plant cell of claim 54, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claims 59-62 (Canceled).

Claim 63 (Previously Presented) A chimeric DNA comprising the following operably linked parts:

- a) a promoter, operative in a plant cell;
- b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences,  
wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence identical to at least 20 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest,

and wherein the second of said annealing RNA sequences comprises an antisense sequence identical to at least 20 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest,

and wherein said DNA region comprises an intron heterologous to said sense sequence; and

- c) a DNA region involved in transcription termination and polyadenylation.

Claim 64 (Previously Presented) A chimeric DNA comprising the following operably linked parts:

- a) a promoter, operative in a plant cell;
- b) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising
  - i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest; and
  - ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 20 consecutive nucleotides of the sense sequence basepair with said at least 20 consecutive nucleotides of the antisense sequence,

wherein said DNA region comprises an intron heterologous to said region with sense nucleotide sequence; and

- c) a DNA region involved in transcription termination and polyadenylation.

Claim 65 (Previously presented) The chimeric DNA of claim 64, wherein said intron is located between part of said DNA region which when transcribed yields said sense

nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 66 (Previously Presented) The chimeric DNA of claim 64, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 67 (Previously Presented) The chimeric DNA of claim 64, wherein said sense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with at least 100 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 100 consecutive nucleotides having 100% sequence identity with the complement of said at least 100 consecutive nucleotides of said sense nucleotide sequence.

Claim 68 (Previously presented) The chimeric DNA of claim 66, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 69 (Previously presented) The chimeric DNA of claim 67, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claims 70-97 (Canceled).

Claim 98 (Withdrawn) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in a plant cell, comprising the



step of introducing into said plant cell a chimeric DNA comprising the following operably linked parts:

- a) a promoter, operative in said plant cell;
- b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences,
  - wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence identical to at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest,
  - and wherein the second of said annealing RNA sequences comprises an antisense sequence identical to at least 20 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest,
  - and wherein said DNA region comprises an intron ; and
- c) a DNA region involved in transcription termination and polyadenylation.

Claim 99 (Withdrawn) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in a plant cell, comprising the step of introducing into said plant cell, a chimeric DNA comprising the following operably linked parts:

- a) a promoter, operative in said plant cell;
- b) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising
  - i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest; and
  - ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 20 consecutive nucleotides of the sense sequence basepair with said at least 20 consecutive nucleotides of the antisense sequence,

and wherein said DNA region comprises an intron ; and

- c) a DNA region involved in transcription termination and polyadenylation.

Claim 100 (Previously Presented) A plant cell, comprising a nucleic acid of interest, which is normally capable of being phenotypically expressed, further comprising a chimeric DNA molecule comprising the following operably linked parts:

- a) a promoter, operative in said plant cell;
- b) a DNA region, which when transcribed, yields an RNA molecule with at least one RNA region with a nucleotide sequence comprising
  - i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of the nucleic acid of interest; and
  - ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence,

and wherein said DNA region comprises an intron ; and

- c) a DNA region involved in transcription termination and polyadenylation.

Claim 101 (Previously presented) A plant comprising the plant cell of claim 100.

Claim 102 (Previously Presented) A chimeric DNA comprising the following operably linked parts:

- a) a promoter, operative in a plant cell;
- b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure comprising two annealing RNA sequences,
  - wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence identical to at least 20 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest, and
  - wherein the second of said annealing RNA sequences comprises an antisense sequence identical to at least 20 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest,
  - and wherein said DNA region comprises an intron; and
- c) a DNA region involved in transcription termination and polyadenylation

Claim 103 (Previously Presented) A chimeric DNA comprising the following operably linked parts:

- a) a promoter, operative in a plant cell;
- b) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising
  - i) a sense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of a nucleic acid of interest; and
  - ii) an antisense nucleotide sequence including at least 20 consecutive nucleotides having 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence;wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 20 consecutive nucleotides of the sense sequence basepair with said at least 20

- consecutive nucleotides of the antisense sequence,  
and wherein said DNA region comprises an intron ; and  
c) a DNA region involved in transcription termination and polyadenylation.

Claims 104-108 (Canceled).

Claim 109 (Previously Presented) The chimeric DNA of claim 64, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequence.

Claim 110 (Canceled).

Claim 111 (Withdrawn) The method of claim 99, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequences.

Claim 112 (Withdrawn) The method of claim 99, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 113 (Withdrawn) The method of claim 99, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 114 (Withdrawn) The method of claim 113, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 115 (Previously Presented) The plant cell of claim 100, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequences.

Claim 116 (Previously Presented) The plant cell of claim 100, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 117 (Previously Presented) The plant cell of claim 100, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 118 (Previously Presented) The plant cell of claim 117, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 119 (Previously Presented) The chimeric DNA of claim 103, wherein said RNA molecule further comprises a spacer nucleotide sequence located between said sense and said antisense nucleotide sequences.

Claim 120 (Previously Presented) The chimeric DNA of claim 103, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claim 121 (Previously Presented) The chimeric DNA of claim 103, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having 100%

sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides having 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

Claim 122 (Previously Presented) The chimeric DNA of claim 121, wherein said intron is located between part of said DNA region which when transcribed yields said sense nucleotide sequence and part of said DNA region which when transcribed yields said antisense nucleotide sequence.

Claims 123-134 (Canceled).